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(54) Title: PLANT VITAMIN E BIOSYNTHETIC ENZYMES

(57) Abstract

This invention relates to an isolated nucleic acid fragment encoding a vitamin E biosynthetic enzyme. The invention also relates to the construction of a chimeric gene encoding all or a portion of the vitamin E biosynthetic enzyme, in sense or antisense orientation, wherein expression of the chimeric gene results in production of altered levels of the vitamin E biosynthetic enzyme in a transformed host cell.

SEQ ID NO:35 RYVVRPKHAL-----TLAFYCYF-----YRTWSS-FGSRSSLLFSP33SSSV-----
SEQ ID NO:40 NKATLAAPSLTSL-P-----YRTWSS-FGSRSSLLFSP33SSSV-----
SEQ ID NO:38 NKN-----SKPA-PLPLHLDAAPPPPSLCHNAAPVPAULPLPAR-KLAAPGV
SEQ ID NO:28 NATVVR-----PTISCIHITHTSOSPTFAIRVGPSPAPIRASA-ASSERGEI
SEQ ID NO:08 NATVVR-----PTISCIHITHTSOSPTFAIRVGPSPAPIRASA-ASSERGEI
SEQ ID NO:22 MANAALLWSSSS-SLAACRCGSSRAPS-VPRSRRLRAVSL--R-PRASSTA
SEQ ID NO:24 AB--VQPTGALATPLRLCTSRHLCAZASPRAGLCLWNRNRSSRRLKLVANMAPT
SEQ ID NO:26 FRH-----GH-----
1
SEQ ID NO:39 ULTHASATIASADLYEKIKMFTDSSCLWEDVNGCKHNGFYCPNGTYE1---DRQDAI
SEQ ID NO:40 AVAAATSTEA--LAKGIAEFYNETSGLMEIINGENHNGFYDSSVLSGSKREAOI
SEQ ID NO:38 VDRPGDAAFFGLKEDIAGLYDSGLMEIINGENHNGFYDSSVLSGSKREAOI
SEQ ID NO:28 VLEQPKKDDKRLKGIAGFYDSSGLMEIINGENHNGFYDSSVLSGSKREAOI
SEQ ID NO:08 VLEQPKKDDKRLKGIAGFYDSSGLMEIINGENHNGFYDSSVLSGSKREAOI
SEQ ID NO:22 ---QAPATAPFGLKEDIAGLYDSGLMEIINGENHNGFYDSSVLSGSKREAOI
SEQ ID NO:24 LSSSTAAAPFGLKEDIAGLYDSGLMEIINGENHNGFYDSSVLSGSKREAOI
SEQ ID NO:26
120
61
SEQ ID NO:39 DLIKELLANVPOESA---KPKKILDGGCGGSSLYLAQOHQAEVGCASLSPVQVRA
SEQ ID NO:40 NKIESLIRAGVTDEK-EKKIKVVDGCGGSSLYLAQOHQAEVGCASLSPVQVRA
SEQ ID NO:38 NKIESLIRAGVTDEK-EKKIKVVDGCGGSSLYLAQOHQAEVGCASLSPVQVRA
SEQ ID NO:28 NKIESLIRAGVTDEK-EKKIKVVDGCGGSSLYLAQOHQAEVGCASLSPVQVRA
SEQ ID NO:08 NKIESLIRAGVTDEK-EKKIKVVDGCGGSSLYLAQOHQAEVGCASLSPVQVRA
SEQ ID NO:22 NKIESLIRAGVTDEK-EKKIKVVDGCGGSSLYLAQOHQAEVGCASLSPVQVRA
SEQ ID NO:24 NKIESLIRAGVTDEK-EKKIKVVDGCGGSSLYLAQOHQAEVGCASLSPVQVRA
SEQ ID NO:26
180
121
SEQ ID NO:39 GERAAAGLGLCTCOFVANALDLPFASDSDVHWSLESGENHPKQAFVGLVVAAPG
SEQ ID NO:40 NDLAAAGLSKASTQVADALDLPFASDSDVHWSLESGENHPKQAFVGLVVAAPG
SEQ ID NO:38 NDLAAAGLSKASTQVADALDLPFASDSDVHWSLESGENHPKQAFVGLVVAAPG
SEQ ID NO:28 NDLAAAGLSKASTQVADALDLPFASDSDVHWSLESGENHPKQAFVGLVVAAPG
SEQ ID NO:08 NDLAAAGLSKASTQVADALDLPFASDSDVHWSLESGENHPKQAFVGLVVAAPG
SEQ ID NO:22 NDLAAAGLSKASTQVADALDLPFASDSDVHWSLESGENHPKQAFVGLVVAAPG
SEQ ID NO:24 NDLAAAGLSKASTQVADALDLPFASDSDVHWSLESGENHPKQAFVGLVVAAPG
SEQ ID NO:26
240
181
SEQ ID NO:39 RLILATVCHNRIPDGNPLTADERNLQAIYDVCLFVSVLPDYATARECGFGEIKTA
SEQ ID NO:40 RTIIVTCHNRILSAGEALQPMQIOLKICKFTYLPANCSTDDYVNLQSHSLQDIKA
SEQ ID NO:38 RTIIVTCHNRILSAGEALQPMQIOLKICKFTYLPANCSTDDYVNLQSHSLQDIKA
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SEQ ID NO:08 RTIIVTCHNRILSAGEALQPMQIOLKICKFTYLPANCSTDDYVNLQSHSLQDIKA
SEQ ID NO:22 RTIIVTCHNRILSAGEALQPMQIOLKICKFTYLPANCSTDDYVNLQSHSLQDIKA
SEQ ID NO:24 RTIIVTCHNRILSAGEALQPMQIOLKICKFTYLPANCSTDDYVNLQSHSLQDIKA
SEQ ID NO:26
300
241
SEQ ID NO:39 DMSVAVPFWHVEISATDPVWALGAGPKTINAALCLLNNHGVKGLVRLGTLGCI
SEQ ID NO:40 DMSVAVPFWHVEISATDPVWALGAGPKTINAALCLLNNHGVKGLVRLGTLGCI
SEQ ID NO:38 DMSVAVPFWHVEISATDPVWALGAGPKTINAALCLLNNHGVKGLVRLGTLGCI
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SEQ ID NO:08 DMSVAVPFWHVEISATDPVWALGAGPKTINAALCLLNNHGVKGLVRLGTLGCI
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SEQ ID NO:24 DMSVAVPFWHVEISATDPVWALGAGPKTINAALCLLNNHGVKGLVRLGTLGCI
SEQ ID NO:26
360
301
SEQ ID NO:39 RPLV-----
SEQ ID NO:40 RPLV-----
SEQ ID NO:38 RPLV-----
SEQ ID NO:28 RPLV-----
SEQ ID NO:08 RPLV-----
SEQ ID NO:22 RPLV-----
SEQ ID NO:24 RPLV-----
SEQ ID NO:26
361
360

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